

# Zheng Zhou

## List of Publications by Year in descending order

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Version: 2024-02-01

21  
papers

704  
citations

686830

13  
h-index

713013

21  
g-index

21  
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21  
docs citations

21  
times ranked

1048  
citing authors

#	ARTICLE	IF	CITATIONS
1	Structural basis of nucleosomal H4K20 methylation by methyltransferase SET8. <i>FASEB Journal</i> , 2022, 36, e22338.	0.2	6
2	Structural basis of nucleosome dynamics modulation by histone variants H2A.B and H2A.Z.2.2. <i>EMBO Journal</i> , 2021, 40, e105907.	3.5	33
3	Recognition of the inherently unstable H2A nucleosome by Swc2 is a major determinant for unidirectional H2A.Z exchange. <i>Cell Reports</i> , 2021, 35, 109183.	2.9	10
4	Molecular basis for the selective recognition and ubiquitination of centromeric histone H3 by yeast E3 ligase Psh1. <i>Journal of Genetics and Genomics</i> , 2021, 48, 463-472.	1.7	7
5	Structural insight into BRCA1-BARD1 complex recruitment to damaged chromatin. <i>Molecular Cell</i> , 2021, 81, 2765-2777.e6.	4.5	44
6	Structural basis for shieldin complex subunit 3-mediated recruitment of the checkpoint protein REV7 during DNA double-strand break repair. <i>Journal of Biological Chemistry</i> , 2020, 295, 250-262.	1.6	21
7	Role of a DEF/Y motif in histone H2A-H2B recognition and nucleosome editing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 3543-3550.	3.3	19
8	Mechanistic and structural insights into histone H2A-H2B chaperone in chromatin regulation. <i>Biochemical Journal</i> , 2020, 477, 3367-3386.	1.7	14
9	NMR investigations on H2A-H2B heterodimer dynamics conferred by histone variant H2A.Z. <i>Biochemical and Biophysical Research Communications</i> , 2019, 518, 752-758.	1.0	3
10	Mutation profile of APP, PSEN1, and PSEN2 in Chinese familial Alzheimer's disease. <i>Neurobiology of Aging</i> , 2019, 77, 154-157.	1.5	27
11	Structural insights into histone chaperone Chz1-mediated H2A.Z recognition and histone replacement. <i>PLoS Biology</i> , 2019, 17, e3000277.	2.6	18
12	Identification of TYR mutations in patients with oculocutaneous albinism. <i>Molecular Medicine Reports</i> , 2018, 17, 8409-8413.	1.1	9
13	Structural basis for recognition of 53BP1 tandem Tudor domain by TIRR. <i>Nature Communications</i> , 2018, 9, 2123.	5.8	35
14	Crystal structure of the histone heterodimer containing histone variant H2A.Bbd. <i>Biochemical and Biophysical Research Communications</i> , 2018, 503, 1786-1791.	1.0	8
15	Two novel mutations in PRPF3 causing autosomal dominant retinitis pigmentosa. <i>Scientific Reports</i> , 2016, 6, 37840.	1.6	11
16	Structural basis of H2A.Z recognition by SRCAP chromatin-remodeling subunit YL1. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 317-323.	3.6	70
17	Anp32e, a higher eukaryotic histone chaperone directs preferential recognition for H2A.Z. <i>Cell Research</i> , 2014, 24, 389-399.	5.7	110
18	Structural basis for recognition of centromere histone variant CenH3 by the chaperone Scm3. <i>Nature</i> , 2011, 472, 234-237.	13.7	119

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19	NMR structure of chaperone Chz1 complexed with histones H2A.Z-H2B. <i>Nature Structural and Molecular Biology</i> , 2008, 15, 868-869.	3.6	87
20	The High-Resolution NMR Structure of the Early Folding Intermediate of the <i>Thermus thermophilus</i> Ribonuclease H. <i>Journal of Molecular Biology</i> , 2008, 384, 531-539.	2.0	19
21	Analysis of protein-folding cooperativity. <i>Nature</i> , 2007, 445, E16-E17.	13.7	34